SEQUENCE LISTING

(1) GENERAL INFORMATION

  (i) APPLICANT: SHERMAN, Linda A.
              LUSTGARTEN, Joseph

 (ii) TITLE OF THE INVENTION: RECOMBINANT CONSTRUCTS ENCODING
          T CELL RECEPTORS SPECIFIC FOR HUMAN HLA-RESTRICTED TUMOR
          ANTIGENS

(iii) NUMBER OF SEQUENCES: 64

 (iv) CORRESPONDENCE ADDRESS:
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   (D) STATE: DC
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   (F) ZIP: 20006-1888

 (v) COMPUTER READABLE FORM:
   (A) MEDIUM TYPE: Diskette
   (B) COMPUTER: IBM Compatible
   (C) OPERATING SYSTEM: DOS
   (D) SOFTWARE: FastSEQ for Windows Version 2.0

 (vi) CURRENT APPLICATION DATA:
   (A) APPLICATION NUMBER: 08/812,393
   (B) FILING DATE: 05-MAR-1997
   (C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:
   (A) APPLICATION NUMBER:
   (B) FILING DATE:

(viii) ATTORNEY/AGENT INFORMATION:
   (A) NAME: Murashige, Kate H
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   (C) REFERENCE/DOCKET NUMBER: 31333-20001.00

 (ix) TELECOMMUNICATION INFORMATION:
   (A) TELEPHONE: 202-887-1500
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   (2) INFORMATION FOR SEQ ID NO:1:

  (i) SEQUENCE CHARACTERISTICS:
   (A) LENGTH: 1350 base pairs
   (B) TYPE: nucleic acid
   (C) STRANDEDNESS: double
   (D) TOPOLOGY: linear

 (ix) FEATURE:

   (A) NAME/KEY: Coding Sequence
   (B) LOCATION: 1...1332
   (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

```
CTC GAG ATG CAG AGG AAC CTG GGA GCT GTG CTG GGG ATT CTG TGG GTG          48
Leu Glu Met Gln Arg Asn Leu Gly Ala Val Leu Gly Ile Leu Trp Val
 1               5                   10                  15

CAG ATT TGC TGG CTG AAA GAA CAG CAA GTG CAG CAG AGT CCC GCA TCC          96
Gln Ile Cys Trp Leu Lys Glu Gln Gln Val Gln Gln Ser Pro Ala Ser
                20                  25                  30

TTG GTT CTG CAG GAG GGG GAG AAC GCA GAG CTC CAG TGT AGC TTT TCC         144
Leu Val Leu Gln Glu Gly Glu Asn Ala Glu Leu Gln Cys Ser Phe Ser
            35                  40                  45

ATC TTT ACA AAC CAG GTG CAG TGG TTT TAC CAA CGT CCT GGG GGA AGA         192
Ile Phe Thr Asn Gln Val Gln Trp Phe Tyr Gln Arg Pro Gly Gly Arg
        50                  55                  60

CTC GTC AGC CTG TTG TAC AAT CCT TCT GGG ACA AAG CAG AGT GGG AGA         240
Leu Val Ser Leu Leu Tyr Asn Pro Ser Gly Thr Lys Gln Ser Gly Arg
65                  70                  75                  80

CTG ACA TCC ACA ACA GTC ATT AAA GAA CGT CGC AGC TCT TTG CAC ATT         288
Leu Thr Ser Thr Thr Val Ile Lys Glu Arg Arg Ser Ser Leu His Ile
                85                  90                  95

TCC TCC TCC CAG ATC ACA GAC TCA GGC ACT TAT CTC TGT GCC TCA AAT         336
Ser Ser Ser Gln Ile Thr Asp Ser Gly Thr Tyr Leu Cys Ala Ser Asn
                100                 105                 110

TCT GGA GGA AGC AAT GCA AAG CTA ACC TTC GGG AAA GGC ACT AAA CTC         384
Ser Gly Gly Ser Asn Ala Lys Leu Thr Phe Gly Lys Gly Thr Lys Leu
            115                 120                 125

TCT GTT AAA TCA GGT GGC GGA GGG TCT GGC GGG GGT GGA TCC GGG GGT         432
Ser Val Lys Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
        130                 135                 140

GGA GGC TCA GAG GCT GCA GTC ACC CAA AGC CCA AGA AAC AAG GTG GCA         480
Gly Gly Ser Glu Ala Ala Val Thr Gln Ser Pro Arg Asn Lys Val Ala
145                 150                 155                 160

GTA ACA GGA GGA AAG GTG ACA TTG AGC TGT AAT CAG ACT AAT AAC CAC         528
Val Thr Gly Gly Lys Val Thr Leu Ser Cys Asn Gln Thr Asn Asn His
                165                 170                 175

AAC AAC ATG TAC TGG TAT CGG CAG GAC ACG GGG CAT GGG CTG AGG CTG         576
Asn Asn Met Tyr Trp Tyr Arg Gln Asp Thr Gly His Gly Leu Arg Leu
                180                 185                 190

ATC CAT TAT TCA TAT GGT GCT GGC AGC ACT GAG AAA GGA GAT ATC CCT         624
Ile His Tyr Ser Tyr Gly Ala Gly Ser Thr Glu Lys Gly Asp Ile Pro
            195                 200                 205

GAT GGA TAC AAG GCC TCC AGA CCA AGC CAA GAG AAC TTC TCC CTC ATT         672
Asp Gly Tyr Lys Ala Ser Arg Pro Ser Gln Glu Asn Phe Ser Leu Ile
        210                 215                 220

CTG GAG TTG GCT ACC CCC TCT CAG ACA TCA GTG TAC TTC TGT GCC AGC         720
Leu Glu Leu Ala Thr Pro Ser Gln Thr Ser Val Tyr Phe Cys Ala Ser
225                 230                 235                 240
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GGT GAG ACA GGG ACC AAC GAA AGA TTA TTT TTC GGT CAT GGA ACC AAG    768
Gly Glu Thr Gly Thr Asn Glu Arg Leu Phe Phe Gly His Gly Thr Lys
            245             250                 255

CTG TCT GTC CTG ACT AGT AAC TCC ATC ATG TAC TTC AGC CAC TTC GTG    816
Leu Ser Val Leu Thr Ser Asn Ser Ile Met Tyr Phe Ser His Phe Val
            260             265                 270

CCG GTC TTC CTG CCA GCG AAG CCC ACC ACG ACG CCA GCG CCG CGA CCA    864
Pro Val Phe Leu Pro Ala Lys Pro Thr Thr Thr Pro Ala Pro Arg Pro
            275             280                 285

CCA ACA CCG GCG CCC ACC ATC GCG TCG CAG CCC CTG TCC CTG CGC CCA    912
Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro
            290             295                 300

TCT AGT TCT AGA GAT CCC AAA CTC TGC TAC CTG CTG GAT GGA ATC CTC    960
Ser Ser Ser Arg Asp Pro Lys Leu Cys Tyr Leu Leu Asp Gly Ile Leu
305             310                 315                 320

TTC ATC TAT GGT GTC ATT CTC ACT GCC TTG TTC CTG AGA GTG AAG TTC   1008
Phe Ile Tyr Gly Val Ile Leu Thr Ala Leu Phe Leu Arg Val Lys Phe
            325             330                 335

AGC AGG AGC GCA GAC GCC CCC GCG TAC CAG CAG GGC CAG AAC CAG CTC   1056
Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu
            340             345                 350

TAT AAC GAG CTC AAT CTA GGA CGA AGA GAG GAG TAC GAT GTT TTG GAC   1104
Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp
            355             360                 365

AAG AGA CGT GGC CGG GAC CCT GAG ATG GGG GGA AAG CCG AGA AGG AAG   1152
Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys
            370             375                 380

AAC CCT CAG GAA GGC CTG TAC AAT GAA CTG CAG AAA GAT AAG ATG GCG   1200
Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala
385             390                 395                 400

GAG GCC TAC AGT GAG ATT GGG ATG AAA GGC GAG CGC CGG AGG GGC AAG   1248
Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys
            405             410                 415

GGG CAC GAT GGC CTT TAC CAG GGT CTC AGT ACA GCC ACC AAG GAC ACC   1296
Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr
            420             425                 430

TAC GAC GCC CTT CAC ATG CAG GCC CTG CCC CCT CGC TAAGCGGCCG CCACCG  1348
Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
            435             440

CG                                                                1350
```

    (2) INFORMATION FOR SEQ ID NO:2:

      (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 444 amino acids
        (B) TYPE: amino acid
        (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

```
Leu Glu Met Gln Arg Asn Leu Gly Ala Val Leu Gly Ile Leu Trp Val
1               5                   10                  15
Gln Ile Cys Trp Leu Lys Glu Gln Gln Val Gln Gln Ser Pro Ala Ser
            20                  25                  30
Leu Val Leu Gln Glu Gly Glu Asn Ala Glu Leu Gln Cys Ser Phe Ser
        35                  40                  45
Ile Phe Thr Asn Gln Val Gln Trp Phe Tyr Gln Arg Pro Gly Gly Arg
    50                  55                  60
Leu Val Ser Leu Leu Tyr Asn Pro Ser Gly Thr Lys Gln Ser Gly Arg
65                  70                  75                  80
Leu Thr Ser Thr Thr Val Ile Lys Glu Arg Arg Ser Ser Leu His Ile
                85                  90                  95
Ser Ser Ser Gln Ile Thr Asp Ser Gly Thr Tyr Leu Cys Ala Ser Asn
            100                 105                 110
Ser Gly Gly Ser Asn Ala Lys Leu Thr Phe Gly Lys Gly Thr Lys Leu
        115                 120                 125
Ser Val Lys Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
        130                 135                 140
Gly Gly Ser Glu Ala Ala Val Thr Gln Ser Pro Arg Asn Lys Val Ala
145                 150                 155                 160
Val Thr Gly Gly Lys Val Thr Leu Ser Cys Asn Gln Thr Asn Asn His
                165                 170                 175
Asn Asn Met Tyr Trp Tyr Arg Gln Asp Thr Gly His Gly Leu Arg Leu
            180                 185                 190
Ile His Tyr Ser Tyr Gly Ala Gly Ser Thr Glu Lys Gly Asp Ile Pro
        195                 200                 205
Asp Gly Tyr Lys Ala Ser Arg Pro Ser Gln Glu Asn Phe Ser Leu Ile
        210                 215                 220
Leu Glu Leu Ala Thr Pro Ser Gln Thr Ser Val Tyr Phe Cys Ala Ser
225                 230                 235                 240
Gly Glu Thr Gly Thr Asn Glu Arg Leu Phe Phe Gly His Gly Thr Lys
                245                 250                 255
Leu Ser Val Leu Thr Ser Asn Ser Ile Met Tyr Phe Ser His Phe Val
                260                 265                 270
Pro Val Phe Leu Pro Ala Lys Pro Thr Thr Thr Pro Ala Pro Arg Pro
        275                 280                 285
Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro
        290                 295                 300
Ser Ser Ser Arg Asp Pro Lys Leu Cys Tyr Leu Leu Asp Gly Ile Leu
305                 310                 315                 320
Phe Ile Tyr Gly Val Ile Leu Thr Ala Leu Phe Leu Arg Val Lys Phe
                325                 330                 335
Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu
        340                 345                 350
Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp
        355                 360                 365
Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys
    370                 375                 380
Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala
385                 390                 395                 400
Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys
                405                 410                 415
Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr
        420                 425                 430
```

Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
    435   440

       (2) INFORMATION FOR SEQ ID NO:3:

     (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 24 base pairs
      (B) TYPE: nucleic acid
      (C) STRANDEDNESS: single
      (D) TOPOLOGY: linear

     (vi) ORIGINAL SOURCE:
      (C) ISOLATE: V-alpha-1

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CCCAAGGCAC TGATGTTCAT CTTC   24

       (2) INFORMATION FOR SEQ ID NO:4:

     (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 27 base pairs
      (B) TYPE: nucleic acid
      (C) STRANDEDNESS: single
      (D) TOPOLOGY: linear

     (vi) ORIGINAL SOURCE:
      (C) ISOLATE: V-alpha-2

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

TGAGACAAAG TCCCCAATCT CTGACAG   27

       (2) INFORMATION FOR SEQ ID NO:5:

     (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 26 base pairs
      (B) TYPE: nucleic acid
      (C) STRANDEDNESS: single
      (D) TOPOLOGY: linear

     (vi) ORIGINAL SOURCE:
      (C) ISOLATE: V-alpha-3

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CTGCAGCTGC TCCTCAAGTA CTATTC   26

       (2) INFORMATION FOR SEQ ID NO:6:

     (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 28 base pairs
      (B) TYPE: nucleic acid
      (C) STRANDEDNESS: single
      (D) TOPOLOGY: linear

     (vi) ORIGINAL SOURCE:
      (C) ISOLATE: V-alpha-4.1.2.3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

TCCCGGAGAA GGTCCACAGT TCCTCTTT   28

        (2) INFORMATION FOR SEQ ID NO:7:

    (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 29 base pairs
      (B) TYPE: nucleic acid
      (C) STRANDEDNESS: single
      (D) TOPOLOGY: linear

    (vi) ORIGINAL SOURCE:
      (C) ISOLATE: V-alpha-4.4

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GAAGCAGCAG AGGGTTTGAA GCCACATAC   29

        (2) INFORMATION FOR SEQ ID NO:8:

    (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 27 base pairs
      (B) TYPE: nucleic acid
      (C) STRANDEDNESS: single
      (D) TOPOLOGY: linear

    (vi) ORIGINAL SOURCE:
      (C) ISOLATE: V-alpha-5

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GGCAGGTCTT CAGTTGCTTA TGAAGGT   27

        (2) INFORMATION FOR SEQ ID NO:9:

    (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 27 base pairs
      (B) TYPE: nucleic acid
      (C) STRANDEDNESS: single
      (D) TOPOLOGY: linear

    (vi) ORIGINAL SOURCE:
      (C) ISOLATE: V-alpha-6

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GGTTCCTCTT CAGGGTCCAG AATATGT   27

        (2) INFORMATION FOR SEQ ID NO:10:

    (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 27 base pairs
      (B) TYPE: nucleic acid
      (C) STRANDEDNESS: single
      (D) TOPOLOGY: linear

    (vi) ORIGINAL SOURCE:
      (C) ISOLATE: V-alpha-7

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

GCGAAGAACT CACCCTGGAC TGTTCAT   27

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:
   (A) LENGTH: 30 base pairs
   (B) TYPE: nucleic acid
   (C) STRANDEDNESS: single
   (D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:
   (C) ISOLATE: V-alpha-8

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GAGCTCCACA GACAACAAGA GGACCGAGCA   30

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:
   (A) LENGTH: 27 base pairs
   (B) TYPE: nucleic acid
   (C) STRANDEDNESS: single
   (D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:
   (C) ISOLATE: V-alpha-9

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GAGCTGCGAC GTTCCTTAGT GACTGTG   27

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:
   (A) LENGTH: 30 base pairs
   (B) TYPE: nucleic acid
   (C) STRANDEDNESS: single
   (D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:
   (C) ISOLATE: V-alpha-10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

CCTCGTCAGC CTGTTGTCCA ATCCTTCTGG   30

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:
   (A) LENGTH: 28 base pairs
   (B) TYPE: nucleic acid
   (C) STRANDEDNESS: single
   (D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:
   (C) ISOLATE: V-alpha-11

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

CAGCCTCATC AATCTGTTCT ACTTGGCT   28

     (2) INFORMATION FOR SEQ ID NO:15:

     (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 28 base pairs
      (B) TYPE: nucleic acid
      (C) STRANDEDNESS: single
      (D) TOPOLOGY: linear

     (vi) ORIGINAL SOURCE:
      (C) ISOLATE: V-alpha-12

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

CCACCAGGGA CCACAGTTTA TCATTCAA   28

     (2) INFORMATION FOR SEQ ID NO:16:

     (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 27 base pairs
      (B) TYPE: nucleic acid
      (C) STRANDEDNESS: single
      (D) TOPOLOGY: linear

     (vi) ORIGINAL SOURCE:
      (C) ISOLATE: V-alpha-14

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

ACCTGGAGAG AATCCTAAGC TCATCAT   27

     (2) INFORMATION FOR SEQ ID NO:17:

     (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 28 base pairs
      (B) TYPE: nucleic acid
      (C) STRANDEDNESS: single
      (D) TOPOLOGY: linear

     (vi) ORIGINAL SOURCE:
      (C) ISOLATE: V-alpha-15

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

AGGTCTTGTG TCCCTGACAG TCCTGGTT   28

     (2) INFORMATION FOR SEQ ID NO:18:

     (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 30 base pairs
      (B) TYPE: nucleic acid
      (C) STRANDEDNESS: single
      (D) TOPOLOGY: linear

     (vi) ORIGINAL SOURCE:
      (C) ISOLATE: V-alpha-16

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

CAAGCAAACA CTGTAGTGCA GAGCCCTTCC   30

     (2) INFORMATION FOR SEQ ID NO:19:

   (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 25 base pairs
    (B) TYPE: nucleic acid
    (C) STRANDEDNESS: single
    (D) TOPOLOGY: linear

   (vi) ORIGINAL SOURCE:
    (C) ISOLATE: V-alpha-17

   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

CAAGACATCC ATAACTGCCC TACAG   25

     (2) INFORMATION FOR SEQ ID NO:20:

   (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 27 base pairs
    (B) TYPE: nucleic acid
    (C) STRANDEDNESS: single
    (D) TOPOLOGY: linear

   (vi) ORIGINAL SOURCE:
    (C) ISOLATE: V-alpha-18

   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

GTGTATGAAA CCCAGGACAG TTCTTAC   27

     (2) INFORMATION FOR SEQ ID NO:21:

   (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 29 base pairs
    (B) TYPE: nucleic acid
    (C) STRANDEDNESS: single
    (D) TOPOLOGY: linear

   (vi) ORIGINAL SOURCE:
    (C) ISOLATE: V-alpha-19

   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

CCGTATTTCT TTCTTATGTT GTTTTGGAT   29

     (2) INFORMATION FOR SEQ ID NO:22:

   (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 28 base pairs
    (B) TYPE: nucleic acid
    (C) STRANDEDNESS: single
    (D) TOPOLOGY: linear

   (vi) ORIGINAL SOURCE:
    (C) ISOLATE: V-alpha-20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

CAAAGCTCTC CATCGCTGAC TGTTCAAG   28

    (2) INFORMATION FOR SEQ ID NO:23:

  (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 23 base pairs
    (B) TYPE: nucleic acid
    (C) STRANDEDNESS: single
    (D) TOPOLOGY: linear

  (vi) ORIGINAL SOURCE:
    (C) ISOLATE: V-beta-1

  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

ATCTAATCCT GGGAAGAGCA AAT   23

    (2) INFORMATION FOR SEQ ID NO:24:

  (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 23 base pairs
    (B) TYPE: nucleic acid
    (C) STRANDEDNESS: single
    (D) TOPOLOGY: linear

  (vi) ORIGINAL SOURCE:
    (C) ISOLATE: V-beta-2

  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

GGCGTCTGGT ACCACGTGGT CAA   23

    (2) INFORMATION FOR SEQ ID NO:25:

  (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 23 base pairs
    (B) TYPE: nucleic acid
    (C) STRANDEDNESS: single
    (D) TOPOLOGY: linear

  (vi) ORIGINAL SOURCE:
    (C) ISOLATE: V-beta-3

  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

GTGAAAGGGC AAGGACAAAA AGC   23

    (2) INFORMATION FOR SEQ ID NO:26:

  (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 22 base pairs
    (B) TYPE: nucleic acid
    (C) STRANDEDNESS: single
    (D) TOPOLOGY: linear

  (vi) ORIGINAL SOURCE:
    (C) ISOLATE: V-beta-4

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

GATATGCGAA CAGTATCTAG GC   22

        (2) INFORMATION FOR SEQ ID NO:27:

    (i) SEQUENCE CHARACTERISTICS:
       (A) LENGTH: 23 base pairs
       (B) TYPE: nucleic acid
       (C) STRANDEDNESS: single
       (D) TOPOLOGY: linear

    (vi) ORIGINAL SOURCE:
       (C) ISOLATE: V-beta-5.1

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

ACATAATCAA AGGAAAGGGA GAA   23

        (2) INFORMATION FOR SEQ ID NO:28:

    (i) SEQUENCE CHARACTERISTICS:
       (A) LENGTH: 23 base pairs
       (B) TYPE: nucleic acid
       (C) STRANDEDNESS: single
       (D) TOPOLOGY: linear

    (vi) ORIGINAL SOURCE:
       (C) ISOLATE: V-beta-6

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

TCCTGATTGG TCAGGAAGGG CAA   23

        (2) INFORMATION FOR SEQ ID NO:29:

    (i) SEQUENCE CHARACTERISTICS:
       (A) LENGTH: 23 base pairs
       (B) TYPE: nucleic acid
       (C) STRANDEDNESS: single
       (D) TOPOLOGY: linear

    (vi) ORIGINAL SOURCE:
       (C) ISOLATE: V-beta-7

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

TACCTGATCA AAAGAATGGG AGA   23

        (2) INFORMATION FOR SEQ ID NO:30:

    (i) SEQUENCE CHARACTERISTICS:
       (A) LENGTH: 23 base pairs
       (B) TYPE: nucleic acid
       (C) STRANDEDNESS: single
       (D) TOPOLOGY: linear

    (vi) ORIGINAL SOURCE:
       (C) ISOLATE: V-beta-8.1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

ATAACCATGA CAATATGTAC TGG   23

      (2) INFORMATION FOR SEQ ID NO:31:

   (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 23 base pairs
    (B) TYPE: nucleic acid
    (C) STRANDEDNESS: single
    (D) TOPOLOGY: linear

   (vi) ORIGINAL SOURCE:
    (C) ISOLATE: V-beta-8.2

   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

ATAACCACAA CAACATGTAC TGG   23

      (2) INFORMATION FOR SEQ ID NO:32:

   (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 23 base pairs
    (B) TYPE: nucleic acid
    (C) STRANDEDNESS: single
    (D) TOPOLOGY: linear

   (vi) ORIGINAL SOURCE:
    (C) ISOLATE: V-beta-8.3

   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

ATAGCCACAA CTACATGTAC TGG   23

      (2) INFORMATION FOR SEQ ID NO:33:

   (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 23 base pairs
    (B) TYPE: nucleic acid
    (C) STRANDEDNESS: single
    (D) TOPOLOGY: linear

   (vi) ORIGINAL SOURCE:
    (C) ISOLATE: V-beta-9

   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

AGCTTGCAAG AGTTGGAAAA CCA   23

      (2) INFORMATION FOR SEQ ID NO:34:

   (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 23 base pairs
    (B) TYPE: nucleic acid
    (C) STRANDEDNESS: single
    (D) TOPOLOGY: linear

   (vi) ORIGINAL SOURCE:
    (C) ISOLATE: V-beta-10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

GATTATGTTT AGCTACAATA ATA   23

      (2) INFORMATION FOR SEQ ID NO:35:

    (i) SEQUENCE CHARACTERISTICS:
     (A) LENGTH: 23 base pairs
     (B) TYPE: nucleic acid
     (C) STRANDEDNESS: single
     (D) TOPOLOGY: linear

    (vi) ORIGINAL SOURCE:
     (C) ISOLATE: V-beta-11

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

ACAAGGTGAC AGGGAAGGGA CAA   23

      (2) INFORMATION FOR SEQ ID NO:36:

    (i) SEQUENCE CHARACTERISTICS:
     (A) LENGTH: 23 base pairs
     (B) TYPE: nucleic acid
     (C) STRANDEDNESS: single
     (D) TOPOLOGY: linear

    (vi) ORIGINAL SOURCE:
     (C) ISOLATE: V-beta-12

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

ACCTACAGAA CCCAAGGACT CAG   23

      (2) INFORMATION FOR SEQ ID NO:37:

    (i) SEQUENCE CHARACTERISTICS:
     (A) LENGTH: 23 base pairs
     (B) TYPE: nucleic acid
     (C) STRANDEDNESS: single
     (D) TOPOLOGY: linear

    (vi) ORIGINAL SOURCE:
     (C) ISOLATE: V-beta-13

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

CAGTTGCCCT CGGATCGATT TTC   23

      (2) INFORMATION FOR SEQ ID NO:38:

    (i) SEQUENCE CHARACTERISTICS:
     (A) LENGTH: 23 base pairs
     (B) TYPE: nucleic acid
     (C) STRANDEDNESS: single
     (D) TOPOLOGY: linear

    (vi) ORIGINAL SOURCE:
     (C) ISOLATE: V-beta-14

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

GCCGAGATCA AGGCTGTGGG CAG   23

      (2) INFORMATION FOR SEQ ID NO:39:

    (i) SEQUENCE CHARACTERISTICS:
     (A) LENGTH: 23 base pairs
     (B) TYPE: nucleic acid
     (C) STRANDEDNESS: single
     (D) TOPOLOGY: linear

    (vi) ORIGINAL SOURCE:
     (C) ISOLATE: V-beta-15

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

AGAACCATCT GTAAGAGTGG AAC   23

      (2) INFORMATION FOR SEQ ID NO:40:

    (i) SEQUENCE CHARACTERISTICS:
     (A) LENGTH: 23 base pairs
     (B) TYPE: nucleic acid
     (C) STRANDEDNESS: single
     (D) TOPOLOGY: linear

    (vi) ORIGINAL SOURCE:
     (C) ISOLATE: V-beta-16

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

CATCAAATAA TAGATATGGG GCA   23

      (2) INFORMATION FOR SEQ ID NO:41:

    (i) SEQUENCE CHARACTERISTICS:
     (A) LENGTH: 23 base pairs
     (B) TYPE: nucleic acid
     (C) STRANDEDNESS: single
     (D) TOPOLOGY: linear

    (vi) ORIGINAL SOURCE:
     (C) ISOLATE: V-beta-17

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

GTAGTCCTGA AAAAGGGCAC ACT   23

      (2) INFORMATION FOR SEQ ID NO:42:

    (i) SEQUENCE CHARACTERISTICS:
     (A) LENGTH: 22 base pairs
     (B) TYPE: nucleic acid
     (C) STRANDEDNESS: single
     (D) TOPOLOGY: linear

    (vi) ORIGINAL SOURCE:
     (C) ISOLATE: V-beta-18

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

CATCTGTCAA AGTGGCACTT CA   22

     (2) INFORMATION FOR SEQ ID NO:43:

       (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 393 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

       (ix) FEATURE:

        (A) NAME/KEY: Coding Sequence
        (B) LOCATION: 1...393
        (D) OTHER INFORMATION:

       (xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

```
ATG AAA TCC TTG AGT GTT TCC CTA GTG GTC CTG TGG CTC CAG TTA AAC      48
Met Lys Ser Leu Ser Val Ser Leu Val Val Leu Trp Leu Gln Leu Asn
 1               5                  10                  15

TGG GTG CAG AGC CAG CAG AAG GTG CAG CAG AGC CCA GAA TCC CTC AGT      96
Trp Val Gln Ser Gln Gln Lys Val Gln Gln Ser Pro Glu Ser Leu Ser
            20                  25                  30

GTC CCA GAG GGA GGC ATG GCC TCT CTC AAC TGC ACT TCA AGT GAT CGC     144
Val Pro Glu Gly Gly Met Ala Ser Leu Asn Cys Thr Ser Ser Asp Arg
        35                  40                  45

AAT TTT CAG TAT TTC TGG TGG TAC AGA CAG CAT TCT GGA GAA GGC CCC     192
Asn Phe Gln Tyr Phe Trp Trp Tyr Arg Gln His Ser Gly Glu Gly Pro
        50                  55                  60

AAA GCA CTG ATG TCC ATC TTC TCT GAT GGT GAC AAG AAA GAA GGC AGA     240
Lys Ala Leu Met Ser Ile Phe Ser Asp Gly Asp Lys Lys Glu Gly Arg
65                  70                  75                  80

TTC ACA GCT CAC CTC AAT AAG GCC AGC CTG CAT GTT TCC CTG CAC ATC     288
Phe Thr Ala His Leu Asn Lys Ala Ser Leu His Val Ser Leu His Ile
            85                  90                  95

AGA GAC TCC CAG CCC AGT GAC TCC GCT CTC TAC TTC TGT GCA GTT ATG     336
Arg Asp Ser Gln Pro Ser Asp Ser Ala Leu Tyr Phe Cys Ala Val Met
            100                 105                 110

GAT TAT AAC CAG GGG AAG CTT ATC TTT GGG CAG GGT ACC AAG TTA TCT     384
Asp Tyr Asn Gln Gly Lys Leu Ile Phe Gly Gln Gly Thr Lys Leu Ser
            115                 120                 125

ATC AAG CCC                                                         393
Ile Lys Pro
    130
```

     (2) INFORMATION FOR SEQ ID NO:44:

       (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 131 amino acids
        (B) TYPE: amino acid

```
    (C)  STRANDEDNESS: single
    (D)  TOPOLOGY: linear

  (ii)  MOLECULE TYPE: protein
  (v)   FRAGMENT TYPE: internal

  (xi)  SEQUENCE DESCRIPTION: SEQ ID NO:44:
```

```
Met Lys Ser Leu Ser Val Ser Leu Val Val Leu Trp Leu Gln Leu Asn
1               5                   10                  15
Trp Val Gln Ser Gln Gln Lys Val Gln Gln Ser Pro Glu Ser Leu Ser
            20                  25                  30
Val Pro Glu Gly Gly Met Ala Ser Leu Asn Cys Thr Ser Ser Asp Arg
        35                  40                  45
Asn Phe Gln Tyr Phe Trp Trp Tyr Arg Gln His Ser Gly Glu Gly Pro
        50                  55                  60
Lys Ala Leu Met Ser Ile Phe Ser Asp Gly Asp Lys Lys Glu Gly Arg
65                  70                  75                  80
Phe Thr Ala His Leu Asn Lys Ala Ser Leu His Val Ser Leu His Ile
                85                  90                  95
Arg Asp Ser Gln Pro Ser Asp Ser Ala Leu Tyr Phe Cys Ala Val Met
            100                 105                 110
Asp Tyr Asn Gln Gly Lys Leu Ile Phe Gly Gln Gly Thr Lys Leu Ser
        115                 120                 125
Ile Lys Pro
130
```

```
        (2)  INFORMATION FOR SEQ ID NO:45:

    (i)  SEQUENCE CHARACTERISTICS:
        (A)  LENGTH: 402 base pairs
        (B)  TYPE: nucleic acid
        (C)  STRANDEDNESS: double
        (D)  TOPOLOGY: linear

  (ix)  FEATURE:

        (A)  NAME/KEY: Coding Sequence
        (B)  LOCATION: 1...402
        (D)  OTHER INFORMATION:

  (xi)  SEQUENCE DESCRIPTION: SEQ ID NO:45:
```

```
ATG GGC TCC AGA CTC TTC TTT GTG GTT TTG ATT CTC CTG TGT GCA AAA    48
Met Gly Ser Arg Leu Phe Phe Val Val Leu Ile Leu Leu Cys Ala Lys
1               5                   10                  15

CAC ATG GAG GCT GCA GTC ACC CAA AGT CCA AGA AGC AAG GTG GCA GTA    96
His Met Glu Ala Ala Val Thr Gln Ser Pro Arg Ser Lys Val Ala Val
            20                  25                  30

ACA GGA GGA AAG GTG ACA TTG AGC TGT CAC CAG ACT AAT AAC CAT GAC    144
Thr Gly Gly Lys Val Thr Leu Ser Cys His Gln Thr Asn Asn His Asp
            35                  40                  45

TAT ATG TAC TGG TAT CGG CAG GAC ACG GGG CAT GGG CTG AGG CTG ATC    192
Tyr Met Tyr Trp Tyr Arg Gln Asp Thr Gly His Gly Leu Arg Leu Ile
        50                  55                  60
```

```
CAT TAC TCA TAT GTC GCT GAC AGC ACG GAG AAA GGA GAT ATC CCT GAT    240
His Tyr Ser Tyr Val Ala Asp Ser Thr Glu Lys Gly Asp Ile Pro Asp
65              70              75              80

GGG TAC AAG GCC TCC AGA CCA AGC CAA GAG AAT TTC TCT CTC ATT CTG    288
Gly Tyr Lys Ala Ser Arg Pro Ser Gln Glu Asn Phe Ser Leu Ile Leu
                85              90              95

GAG TTG GCT TCC CTT TCT CAG TCA GCT GTA TAT TTC TGT GCG AGC AGC    336
Glu Leu Ala Ser Leu Ser Gln Ser Ala Val Tyr Phe Cys Ala Ser Ser
                100             105             110

GAT TTC GCC GGG ACA GGG GGC TTC TAT GAA CAG TAC TTC GGT CCC GGC    384
Asp Phe Ala Gly Thr Gly Gly Phe Tyr Glu Gln Tyr Phe Gly Pro Gly
        115             120             125

ACC AGG CTC ACG GTT TCT                                             402
Thr Arg Leu Thr Val Ser
    130
```

        (2) INFORMATION FOR SEQ ID NO:46:

            (i) SEQUENCE CHARACTERISTICS:
                (A) LENGTH: 134 amino acids
                (B) TYPE: amino acid
                (C) STRANDEDNESS: single
                (D) TOPOLOGY: linear

            (ii) MOLECULE TYPE: protein
            (v) FRAGMENT TYPE: internal

            (xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

```
Met Gly Ser Arg Leu Phe Phe Val Val Leu Ile Leu Leu Cys Ala Lys
1               5               10              15
His Met Glu Ala Ala Val Thr Gln Ser Pro Arg Ser Lys Val Ala Val
            20              25              30
Thr Gly Gly Lys Val Thr Leu Ser Cys His Gln Thr Asn Asn His Asp
        35              40              45
Tyr Met Tyr Trp Tyr Arg Gln Asp Thr Gly His Gly Leu Arg Leu Ile
    50              55              60
His Tyr Ser Tyr Val Ala Asp Ser Thr Glu Lys Gly Asp Ile Pro Asp
65              70              75              80
Gly Tyr Lys Ala Ser Arg Pro Ser Gln Glu Asn Phe Ser Leu Ile Leu
                85              90              95
Glu Leu Ala Ser Leu Ser Gln Ser Ala Val Tyr Phe Cys Ala Ser Ser
                100             105             110
Asp Phe Ala Gly Thr Gly Gly Phe Tyr Glu Gln Tyr Phe Gly Pro Gly
        115             120             125
Thr Arg Leu Thr Val Ser
    130
```

        (2) INFORMATION FOR SEQ ID NO:47:

            (i) SEQUENCE CHARACTERISTICS:
                (A) LENGTH: 9 amino acids
                (B) TYPE: amino acid
                (C) STRANDEDNESS: single
                (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

Lys Ile Phe Gly Ser Leu Ala Phe Leu
1   5

      (2) INFORMATION FOR SEQ ID NO:48:

      (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 10 amino acids
        (B) TYPE: amino acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

Thr Leu Gln Gly Leu Gly Ile Ser Trp Leu
1   5   10

      (2) INFORMATION FOR SEQ ID NO:49:

      (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 10 amino acids
        (B) TYPE: amino acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

Val Met Ala Gly Val Gly Ser Pro Tyr Val
1   5   10

      (2) INFORMATION FOR SEQ ID NO:50:

      (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 10 amino acids
        (B) TYPE: amino acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

Val Leu Gln Gly Leu Pro Arg Glu Tyr Val
1   5   10

      (2) INFORMATION FOR SEQ ID NO:51:

      (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 8 amino acids
        (B) TYPE: amino acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

His Leu Tyr Gln Gly Gln Trp
1   5

(2) INFORMATION FOR SEQ ID NO:52:

  (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 9 amino acids
    (B) TYPE: amino acid
    (C) STRANDEDNESS: single
    (D) TOPOLOGY: linear

  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

Arg Leu Leu Gln Glu Thr Glu Leu Val
1   5

(2) INFORMATION FOR SEQ ID NO:53:

  (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 9 amino acids
    (B) TYPE: amino acid
    (C) STRANDEDNESS: single
    (D) TOPOLOGY: linear

  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

Lys Ile Pro Val Ala Ile Lys Val Leu
1   5

(2) INFORMATION FOR SEQ ID NO:54:

  (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 9 amino acids
    (B) TYPE: amino acid
    (C) STRANDEDNESS: single
    (D) TOPOLOGY: linear

  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

Cys Leu Thr Ser Thr Val Gln Leu Val
1   5

(2) INFORMATION FOR SEQ ID NO:55:

  (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 9 amino acids
    (B) TYPE: amino acid
    (C) STRANDEDNESS: single
    (D) TOPOLOGY: linear

  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

Gln Leu Met Pro Tyr Gly Cys Leu Leu
1   5

(2) INFORMATION FOR SEQ ID NO:56:

  (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 9 amino acids
    (B) TYPE: amino acid
    (C) STRANDEDNESS: single
    (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

Val Leu Val Lys Ser Pro Asn His Val
  1   5

        (2) INFORMATION FOR SEQ ID NO:57:

        (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 9 amino acids
          (B) TYPE: amino acid
          (C) STRANDEDNESS: single
          (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

Asp Ile Asp Glu Thr Glu Tyr His Ala
  1   5

        (2) INFORMATION FOR SEQ ID NO:58:

        (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 9 amino acids
          (B) TYPE: amino acid
          (C) STRANDEDNESS: single
          (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

Asp Leu Leu Glu Lys Gly Glu Arg Leu
  1   5

        (2) INFORMATION FOR SEQ ID NO:59:

        (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 9 amino acids
          (B) TYPE: amino acid
          (C) STRANDEDNESS: single
          (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

Glu Leu Val Ser Glu Phe Ser Arg Met
  1   5

        (2) INFORMATION FOR SEQ ID NO:60:

        (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 10 amino acids
          (B) TYPE: amino acid
          (C) STRANDEDNESS: single
          (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

Glu Leu Val Ser Glu Phe Ser Arg Met Ala
  1   5   10

(2) INFORMATION FOR SEQ ID NO:61:

    (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 9 amino acids
      (B) TYPE: amino acid
      (C) STRANDEDNESS: single
      (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

Leu Val Ser Glu Phe Ser Arg Met Ala
1   5

(2) INFORMATION FOR SEQ ID NO:62:

    (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 9 amino acids
      (B) TYPE: amino acid
      (C) STRANDEDNESS: single
      (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

Asp Leu Val Asp Ala Glu Glu Tyr Leu
1   5

(2) INFORMATION FOR SEQ ID NO:63:

    (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 9 amino acids
      (B) TYPE: amino acid
      (C) STRANDEDNESS: single
      (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

Thr Leu Ser Pro Gly Lys Asn Gly Val
1   5

(2) INFORMATION FOR SEQ ID NO:64:

    (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 9 amino acids
      (B) TYPE: amino acid
      (C) STRANDEDNESS: single
      (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

Lys Leu Val Gly Lys Leu Asn Trp Ala
1   5